

O/PE

2/3/2001

Serial Number: 09/865,993

CRF Processing Date:

Edited by:

Verified by:

(STIC staff)

ENTERED

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☒ Deleted extra, invalid, headings used by an applicant, specifically: C2207 in seq. 3
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/865,993

DATE: 07/03/2001

TIME: 17:21:54

Input Set : A:\Pto.amc

Output Set: N:\CRF3\07032001\I865993.raw

6 <110> APPLICANT: Brett P. Monia
7 Andrew T. Watt
9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF DUAL SPECIFIC PHOSPHATASE 5
EXPRESSION
11 <130> FILE REFERENCE: RTS-0175
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/865,993
C--> 13 <141> CURRENT FILING DATE: 2001-05-25
13 <160> NUMBER OF SEQ ID NOS: 89
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 20
18 <212> TYPE: DNA
19 <213> ORGANISM: Artificial Sequence
21 <220> FEATURE:
23 <223> OTHER INFORMATION: Antisense Oligonucleotide
25 <400> SEQUENCE: 1
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29 <210> SEQ ID NO: 2
30 <211> LENGTH: 20
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial Sequence
34 <220> FEATURE:
36 <223> OTHER INFORMATION: Antisense Oligonucleotide
38 <400> SEQUENCE: 2
39 atgcattctg cccccaagga 20
42 <210> SEQ ID NO: 3
43 <211> LENGTH: 2139
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
48 <220> FEATURE:
49 <221> NAME/KEY: CDS
50 <222> LOCATION: (47)...(1201)
52 <400> SEQUENCE: 3
53 cgcggggcgc gcggcgcggg gcggcctggc cggcgggcggc ggcggc atg aag gtc 55
54 Met Lys Val
55 1
57 acg tcg ctc gac ggg cgc cag ctg cgc aag atg ctc cgc aag gag gcg 103
58 Thr Ser Leu Asp Gly Arg Gln Leu Arg Lys Met Leu Arg Lys Glu Ala
59 5 10 15
61 gcg gcg cgc tgc gtg gtg ctc gac tgc cgg ccc tat ctg gcc ttc gct 151
62 Ala Ala Arg Cys Val Val Leu Asp Cys Arg Pro Tyr Leu Ala Phe Ala
63 20 25 30 35
65 gcc tcg aac gtg cgc ggc tcg ctc aac gtc aac ctc aac tcg gtg gtg 199
66 Ala Ser Asn Val Arg Gly Ser Leu Asn Val Asn Leu Asn Ser Val Val
67 40 45 50
69 ctg cgg cgg gcc cgg ggc ggc gcg gtg tcg gcg cgc tac gtg ctg ccc 247
70 Leu Arg Arg Ala Arg Gly Gly Ala Val Ser Ala Arg Tyr Val Leu Pro
71 55 60 65
73 gac gag gcg gcg cgc gcg cgg ctc ctg cag gag ggc ggc ggc ggc gtc 295

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75			70					75				80					
77	gcg	gcc	gtg	gtg	gtg	ctg	gac	cag	ggc	agc	cgc	cac	tgg	cag	aag	ctg	343
78	Ala	Ala	Val	Val	Val	Leu	Asp	Gln	Gly	Ser	Arg	His	Trp	Gln	Lys	Leu	
79		85					90					95					
81	cga	gag	gag	agc	gcc	gcg	cgt	gtc	gtc	ctc	acc	tcg	cta	ctc	gct	tgc	391
82	Arg	Glu	Glu	Ser	Ala	Ala	Arg	Val	Val	Leu	Thr	Ser	Leu	Leu	Ala	Cys	
83	100					105					110					115	
85	cta	ccc	gcc	ggc	ccg	cgg	gtc	tac	ttc	ctc	aaa	ggg	gga	tat	gag	act	439
86	Leu	Pro	Ala	Gly	Pro	Arg	Val	Tyr	Phe	Leu	Lys	Gly	Gly	Tyr	Glu	Thr	
87					120					125					130		
89	ttc	tac	tcg	gaa	tat	cct	gag	tgt	tgc	gtg	gat	gta	aaa	ccc	att	tca	487
90	Phe	Tyr	Ser	Glu	Tyr	Pro	Glu	Cys	Cys	Val	Asp	Val	Lys	Pro	Ile	Ser	
91			135					140					145				
93	caa	gag	aag	att	gag	agt	gag	aga	gcc	ctc	atc	agc	cag	tgt	gga	aaa	535
94	Gln	Glu	Lys	Ile	Glu	Ser	Glu	Arg	Ala	Leu	Ile	Ser	Gln	Cys	Gly	Lys	
95		150					155					160					
97	cca	gtg	gta	aat	gtc	agc	tac	agg	cca	gct	tat	gac	cag	ggg	ggc	cca	583
98	Pro	Val	Val	Asn	Val	Ser	Tyr	Arg	Pro	Ala	Tyr	Asp	Gln	Gly	Gly	Pro	
99		165				170					175						
101	gtt	gaa	atc	ctt	ccc	ttc	ctc	tac	ctt	gga	agt	gcc	tac	cat	gca	tcc	631
102	Val	Glu	Ile	Leu	Pro	Phe	Leu	Tyr	Leu	Gly	Ser	Ala	Tyr	His	Ala	Ser	
103	180					185				190					195		
105	aag	tgc	gag	ttc	ctc	gcc	aac	ttg	cac	atc	aca	gcc	ctg	ctg	aat	gtc	679
106	Lys	Cys	Glu	Phe	Leu	Ala	Asn	Leu	His	Ile	Thr	Ala	Leu	Leu	Asn	Val	
107				200					205				210				
109	tcc	cga	cgg	acc	tcc	gag	gcc	tgc	atg	acc	cac	cta	cac	tac	aaa	tgg	727
110	Ser	Arg	Arg	Thr	Ser	Glu	Ala	Cys	Met	Thr	His	Leu	His	Tyr	Lys	Trp	
111			215					220				225					
113	atc	cct	gtg	gaa	gac	agc	cac	acg	gct	gac	att	agc	tcc	cac	ttt	caa	775
114	Ile	Pro	Val	Glu	Asp	Ser	His	Thr	Ala	Asp	Ile	Ser	Ser	His	Phe	Gln	
115		230					235				240						
117	gaa	gca	ata	gac	ttc	att	gac	tgt	gtc	agg	gaa	aag	gga	ggc	aag	gtc	823
118	Glu	Ala	Ile	Asp	Phe	Ile	Asp	Cys	Val	Arg	Glu	Lys	Gly	Gly	Lys	Val	
119		245				250			255								
121	ctg	gtc	cac	tgt	gag	gct	ggg	atc	tcc	cgt	tca	ccc	acc	atc	tgc	atg	871
122	Leu	Val	His	Cys	Glu	Ala	Gly	Ile	Ser	Arg	Ser	Pro	Thr	Ile	Cys	Met	
123	260				265				270						275		
125	gct	tac	ctt	atg	aag	acc	aag	cag	ttc	cgc	ctg	aag	gag	gcc	ttc	gat	919
126	Ala	Tyr	Leu	Met	Lys	Thr	Lys	Gln	Phe	Arg	Leu	Lys	Glu	Ala	Phe	Asp	
127			280				285				290						
129	tac	atc	aag	cag	agg	agg	agc	atg	gtc	tcg	ccc	aac	ttt	ggc	ttc	atg	967
130	Tyr	Ile	Lys	Gln	Arg	Arg	Ser	Met	Val	Ser	Pro	Asn	Phe	Gly	Phe	Met	
131			295				300				305						
133	ggc	cag	ctc	ctg	cag	tac	gaa	tct	gag	atc	ctg	ccc	tcc	acg	ccc	aac	1015
134	Gly	Gln	Leu	Leu	Gln	Tyr	Glu	Ser	Glu	Ile	Leu	Pro	Ser	Thr	Pro	Asn	
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137	ccc	cag	cct	ccc	tcc	tgc	caa	ggg	gag	gca	gca	ggc	tct	tca	ctg	ata	1063
138	Pro	Gln	Pro	Pro	Ser	Cys	Gln	Gly	Glu	Ala	Ala	Gly	Ser	Ser	Leu	Ile	

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142 Gly His Leu Gln Thr Leu Ser Pro Asp Met Gln Gly Ala Tyr Cys Thr
143 340      345      350      355
145 ttc cct gcc tcg gtg ctg gca ccg gtg cct acc cac tca aca gtc tca      1159
146 Phe Pro Ala Ser Val Leu Ala Pro Val Pro Thr His Ser Thr Val Ser
147      360      365      370
149 gag ctc agc aga agc cct gtg gca acg gcc aca tcc tgc taa aactgggatg 1211
150 Glu Leu Ser Arg Ser Pro Val Ala Thr Ala Thr Ser Cys
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153 gaggaatcgg cccagcccca agagcaactg tgatttttgt ttttaagact catggacatt 1271
155 tcataacctga tgcaatactg aagacctcat tctgtcatgc tgccccagtg agatagttag 1331
157 tggtcaccag gcttgcaaat gaacttcaga cggacctcag ggtaggttct cgggactgaa 1391
159 ggaaggccaa gccattacgg gagcacagca tgtgtgtgact actgtacttc cagacccttg 1451
161 cctccttggg actgcccagt ccttgcacct cagagttcgc cttttcattt caagcataag 1511
163 gcaataaata cctgcagcaa cgtgggagaa agaagttgct ggaccaggag aaaaggcagt 1571
165 tatgaagcca attcattttg aaggaagcac aatttccacc ttattttttg aactttggca 1631
167 gtttcaatgt ctgtctctgt tgcttcgggg cataagctga tcaccgtcta gttgggaaag 1691
169 taaccctaca gggttttagt ggacatgatc agcatcctga tttgaacct gaaatgttgt 1751
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175 acttgaactt gtctcattcc acctcttctc agagcaactc ttcctttggg aaaagagttc 1931
177 ttcagatcat agacaaaaaa agtcatacct tcgaggtggt agcagtagat tccaggagga 1991
179 gaagggtact tgctaggtat cctgggtcag tggcggtgca aactggtttc ctcagctgcc 2051
181 tgtccttctg tgtgcttatg tctcttgtga caattgtttt cctccctgcc cctggaggtt 2111
183 gtcttcaagc tgtggacttc tgggattt      2139
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189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE:
193 <223> OTHER INFORMATION: PCR Primer
195 <400> SEQUENCE: 4
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199 <210> SEQ ID NO: 5
200 <211> LENGTH: 25
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202 <213> ORGANISM: Artificial Sequence
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208 <400> SEQUENCE: 5
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213 <211> LENGTH: 23
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial Sequence
217 <220> FEATURE:
219 <223> OTHER INFORMATION: PCR Probe
221 <400> SEQUENCE: 6

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232 <223> OTHER INFORMATION: PCR Primer
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238 <210> SEQ ID NO: 8
239 <211> LENGTH: 20
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
245 <223> OTHER INFORMATION: PCR Primer
247 <400> SEQUENCE: 8
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252 <211> LENGTH: 20
253 <212> TYPE: DNA
254 <213> ORGANISM: Artificial Sequence
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258 <223> OTHER INFORMATION: PCR Probe
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277 tgcctcgccc gcggaacccc tggcctgga caccctggcc gtgggcaccc gcggggcgcg 180
279 cggcgcgggg ccgctggcgg gcggcgggcg cggcatgaag gtcacgtcgc tcgacgggcg 240
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283 gccctatctg gccctcgctg cctcgaacgt gcgcggctcg ctcaacgtca acctcaactc 360
285 ggtggtgctg cggcgggccc gggcgggcgc ggtgtcggcg cgctacgtgc tgcccgaaga 420
287 ggcggcgcgc gcgcggctcc tgcaggaggc cggcgggcgc gtcgcggccg tgggtggtgct 480
289 ggaccagggc agccgccact ggcagaagct gcgagaggag agcgcgcgcg gtgtcgtcct 540
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293 tgagactttc tactcggaat atcctgagtg ttgcgtggat gtaaaaccca ttccacaaga 660
295 gaagattgag agtgagagag ccctcatcag ccagtgtgga aaaccagtgg taaatgtcag 720
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299 aagtgcctac catgcatcca agtgcgagtt cctcgccaac ttgcacatca cagccctgct 840
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305 tgactgtgtc agggaaaagg gaggcaaggc cctggtccac tgtgaggctg ggatctcccg 1020
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319 aggaatcggc ccagccccaa gagcaactgt gattttttgt tttaagactc atggacattt 1440
321 catacctgat gcaatactga agacctcatt ctgtcatgct gccccagtga gatagttagt 1500
323 ggtcaccagg cttgcaaatt aacttcagac ggacctcagg gtaggttctc gggactgaag 1560
325 gaaggccaag ccattacggg agcacagcat gtgctgacta ctgtacttcc agaccctgc 1620
327 cctcttgga ctgcccagtc cttgcacctc agagttcgcc ttttcatttc aagcataagg 1680
329 caataaatac ctgcagcaac gtgggagaaa gaagttgctg gaccaggaga aaaggcagtt 1740
331 atgaagccaa ttcattttga aggaagcaca atttccacct tattttttga actttggcag 1800
333 tttcaatgtc tgtctctgtt gcttcggggc ataagctgat caccgtctag ttgggaaagt 1860
335 aacctacag ggtttgtagg gacatgatca gcatcctgat ttgaacctg aaatgttgtg 1920
337 tagacaccct cttgggtcca atgaggtagt tggttgaagt agcaagatgt tggcttttct 1980
339 ggattttttt tgccatgggt tcttcaactga ccttggaact tggcatgatt cttagtata 2040
341 cttgaacttg tctcattcca cctcttctca gagcaactct tcctttggga aaagagttct 2100
343 tcagatcata gacaaaaaaa gtcatacctt cgaggtggtg gcagtagatt ccaggaggag 2160
345 aagggtactt gctaggtatc ctgggtcagt ggcggtgcaa actggtttcc tcagctgcct 2220
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358 <210> SEQ ID NO: 11

359 <211> LENGTH: 475

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361 <213> ORGANISM: Homo sapiens

363 <220> FEATURE:

366 <400> SEQUENCE: 11

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371 ggcattgaag tcacgtcgtc cgacgggcgc cagctgcgca agatgctccg caaggaggcg 180
373 gcgcgcgcgt gcgtggtgct cgactgccgc ccctatctgg ccttcgtgc ctgcaacgtg 240
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377 gtgtcggcgc gctacgtgct ggaccagggc agccgccact ggcagaagct gcgagaggag 360
379 agcgcgcgcg gtgtcgtcct caccctgcta ctgcttgcc taccgcgcg cccgcgggtc 420
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387 <213> ORGANISM: Artificial Sequence

389 <220> FEATURE:

391 <223> OTHER INFORMATION: Antisense Oligonucleotide

393 <400> SEQUENCE: 12

394 gacgtgacct tcatgccgcc

20

397 <210> SEQ ID NO: 13

398 <211> LENGTH: 20

399 <212> TYPE: DNA

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3